AMENDMENTS TO THE CLAIMS:

Claims 180-193 are added. Claims 118-179 were previously pending. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-117 (Canceled.)

Claim 118. (Previously presented.) A nucleic acid encoding a variant of a parent *Bacillus stearothermophilus* alpha-amylase, wherein the variant has an amino acid sequence which has at least 95% homology to the parent *Bacillus stearothermophilus* alpha-amylase and comprises a deletion of amino acids 179 and 180, using SEQ ID NO:3 for numbering, and wherein the variant has alpha-amylase activity

Claim 119. (Previously presented.) The nucleic acid of claim 118, wherein the variant further comprises a substitution of a cysteine at amino acids 349 and 428, using SEQ ID NO:3 for numbering.

Claim 120. (Previously presented.) A nucleic acid construct comprising the nucleic acid of claim 118 operably linked to one or more control sequences that direct the production of the variant in a suitable expression host.

Claim 121. (Previously presented.) The nucleic acid construct of claim 120, wherein one or more control sequence directs the production of the variant in a bacterial host.

Claim 122. (Previously presented.) The nucleic acid construct of claim 120, wherein one or more control sequence directs the production of the variant in a fungal host.

Claim 123. (Previously presented.) A recombinant expression vector comprising the nucleic acid construct of claim 120.

Claim 124. (Previously presented.) A recombinant host cell comprising the nucleic acid construct of claim 120.

Claim 125. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is a bacterial cell.

Claim 126. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is a fungal cell.

Claim 127. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is a yeast cell.

Claim 128. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is a species of *Bacillus*.

Claim 129. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 130. (Previously presented.) The recombinant host cell of claim 124, wherein the host cell is *Bacillus licheniformis*.

Claim 131. (Previously presented.) A method for producing a variant alpha-amylase, which method comprises: (a) cultivating a host cell comprising the nucleic acid of claim 118 and (b) recovering the variant alpha-amylase from the host cell.

Claim 132. (Previously presented.) The method of claim 131, wherein the host cell is a bacterial cell.

Claim 133. (Previously presented.) The method of claim 131, wherein the host cell is a fungal cell.

Claim 134. (Previously presented.) The method of claim 131, wherein the host cell is a yeast cell.

Claim 135. (Previously presented.) The method of claim 131, wherein the host cell is a species of *Bacillus*.

Claim 136. (Previously presented.) The method of claim 131, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 137. (Previously presented.) The method of claim 131, wherein the host cell is *Bacillus licheniformis*.

Claim 138. (Previously presented.) The method of claim 131, wherein the variant alpha-amylase is secreted from the host cell.

Claim 139. (Previously presented.) A nucleic acid encoding a variant alpha-amylase, wherein the variant has at least 95% homology to SEQ ID NO:3 and comprises a deletion of amino acids 179 and 180, using SEQ ID NO:3 for numbering, and wherein the variant has alpha-amylase activity.

Claim 140. (Previously presented.) A nucleic acid of claim 139, wherein the variant further comprises a substitution of a cysteine at amino acids 349 and 428, using SEQ ID NO:3 for numbering.

Claim 141. (Previously presented.) A nucleic acid construct comprising the nucleic acid of claim 139 operably linked to one or more control sequences that direct the production of the variant in a suitable expression host.

Claim 142. (Previously presented.) A nucleic acid construct of claim 141, wherein one or more control sequence directs the production of the variant in a bacterial host.

Claim 143. (Previously presented.) A nucleic acid construct of claim 141, wherein one or more control sequence directs the production of the variant in a fungal host

Claim 144. (Previously presented.) A recombinant expression vector comprising the nucleic acid of claim 139.

Claim 145. (Previously presented.) A recombinant host cell comprising the nucleic acid construct of claim 141.

Claim 146. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is a bacterial cell.

Claim 147. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is a fungal cell.

Claim 148. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is a yeast cell.

Claim 149. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is a species of *Bacillus*.

Claim 150. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 151. (Previously presented.) The recombinant host cell of claim 145, wherein the host cell is *Bacillus licheniformis*.

Claim 152. (Previously presented.) A method for expressing a variant alpha-amylase, which method comprises: (a) cultivating a host cell comprising the nucleic acid of claim 139 and (b) recovering the variant alpha-amylase from the host cell.

Claim 153. (Previously presented.) The method of claim 152, wherein the host cell is a bacterial cell.

Claim 154. (Previously presented.) The method of claim 152, wherein the host cell is a fungal cell.

Claim 155. (Previously presented.) The method of claim 152, wherein the host cell is a yeast cell.

Claim 156. (Previously presented.) The method of claim 152, wherein the host cell is a species of *Bacillus*.

Claim 157. (Previously presented.) The method of claim 152, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 158. (Previously presented.) The method of claim 152, wherein the host cell is *Bacillus licheniformis*.

Claim 159. (Previously presented.) The method of claim 152, wherein the variant alpha-amylase is secreted from the host cell.

Clam 160. (Previously presented.) A nucleic acid sequence encoding a variant of a *Bacillus stearothermophilus* alpha-amylase, wherein the alpha-amylase variant consists of a deletion of amino acids 179 and 180, using SEQ ID NO:3 for numbering.

Claim 161. (Previously presented.) A nucleic construct comprising the nucleic sequence of claim 160 operably linked to one or more control sequence that direct the production of the variant in a suitable expression host.

Claim 162. (Previously presented.) The nucleic acid construct of claim 161, wherein one or more control sequences directs the production of the variant in a bacterial host.

Claim 163. (Previously presented.) The nucleic acid construct of claim 161, wherein one or more control sequence directs the production of the variant in a fungal host.

Claim 164. (Previously presented.) A recombinant expression vector comprising the nucleic acid construct of claim 161.

Claim 165. (Previously presented.) A recombinant host cell comprising the nucleic construct of claim 161.

Claim 166. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is a bacterial cell.

Claim 167. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is a fungal cell.

Claim 168. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is a yeast cell.

Claim 169. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is a species of *Bacillus*.

Claim 170. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 171. (Previously presented.) The recombinant host cell of claim 165, wherein the host cell is *Bacillus licheniformis*.

Claim 172. (Previously presented.) A method for producing a variant alpha-amylase, which method comprises: (a) cultivating a host cell comprising the nucleic acid of claim 160 and (b) recovering the variant alpha-amylase from the host cell.

Claim 173. (Previously presented.) The method of claim 172, wherein the host cell is a bacterial cell.

Claim 174. (Previously presented.) The method of claim 172, wherein the host cell is a fungal cell.

Claim 175. (Previously presented.) The method of claim 172, wherein the host cell is a yeast cell.

Claim 176. (Previously presented.) The method of claim 172, wherein the host cell is a species of *Bacillus*.

Claim 177. (Previously presented.) The method of claim 172, wherein the host cell is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Bacillus thuringiensis*, *Streptomyces lividans* and *Streptomyces murinus*.

Claim 178. (Previously presented.) The method of claim 172, wherein the host cell is *Bacillus licheniformis*.

Claim 179. (Previously presented.) The method of claim 172, wherein the variant alpha-amylase is secreted from the host cell.

Claim 180. (New.) A method for producing ethanol from starch, comprising:

a) treating starch with an alpha-amylase, wherein the alpha-amylase is selected from the group consisting of an alpha-amylase comprising an amino acid sequence having at least 80% homology to SEQ ID NO:1 and which alpha-amylase is modified by having an amino acid deletion of two amino acids selected from the group of amino acids equivalent to positions 180, 181, 182, 183, 184 and 185 in SEQ ID NO:1; and

b) preparing ethanol from the treated starch.

Claim 181. (New.) A method for producing ethanol from starch, comprising:

a) treating starch with an alpha-amylase, wherein the alpha-amylase is selected from the group consisting of an alpha-amylase comprising an amino acid sequence having at least 80% homology to SEQ ID NO:2 and which alpha-amylase is modified by having an amino acid

deletion of two amino acids selected from the group of amino acids equivalent to positions 180, 181, 182, 183, 184 and 185 in SEQ ID NO:2; and

b) preparing ethanol from the treated starch.

Claim 182. (New.) A method for producing ethanol from starch, comprising:

a) treating starch with an alpha-amylase, wherein the alpha-amylase is selected from the group consisting of an alpha-amylase comprising an amino acid sequence having at least 80% homology to SEQ ID NO:3 and which alpha-amylase is modified by having an amino acid deletion of two amino acids selected from the group of amino acids equivalent to positions 178, 179, 180, 181, 182 and 183 in SEQ ID NO:3; and

b) preparing ethanol from the treated starch.

Claim 183. (New.) A method for producing ethanol from starch, comprising:

a) treating starch with an alpha-amylase, wherein the alpha-amylase is selected from the group consisting of an alpha-amylase comprising an amino acid sequence having at least 80% homology to SEQ ID NO:7 and which alpha-amylase is modified by having an amino acid deletion of two amino acids selected from the group of amino acids equivalent to positions 180, 181, 182, 183, 184 and 185 in SEQ ID NO:7; and

b) preparing ethanol from the treated starch.

Claim 184. (New.) The method of claim 182, wherein the alpha amylase comprises a deletion of three amino acids selected from the group of amino acids equivalent to positions 178, 179, 180, 181, 182 and 183 in SEQ ID NO:3.

Claim 185. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 179 and 180 in SEQ ID NO. 3.

Claim 186. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 181 and 182 in SEQ ID NO. 3.

Claim 187. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 179 and 181 in SEQ ID NO. 3.

Claim 188. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 180 and 181 in SEQ ID NO. 3.

Claim 189. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 180 and 182 in SEQ ID NO. 3.

Claim 190. (New.) The method of claim 182, wherein the alpha-amylase comprises a deletion at positions equivalent to positions 179 and 182 in SEQ ID NO. 3.

Claim 191. (New.) The method of claim 182, wherein the alpha-amylase comprises an amino acid sequence having at least 85% homology to SEQ ID NO:3.

Claim 192. (New.) The method of claim 182, wherein the alpha-amylase comprises an amino acid sequence having at least 90% homology to SEQ ID NO:3.

Claim 193. (New.) The method of claim 182, wherein the alpha-amylase comprises an amino acid sequence having at least 95% homology to SEQ ID NO:3.